Single Cell Gene Expression Profiling of Skeletal Muscle-Derived Cells.

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Public Summary:
It is challenging to understand the behavior of a heterogeneous cellular population. Since each cell is a separate entity, we have undertaken an effort to isolate the skeletal muscle cells termed Fibro-Adipogenic Progenitors (FAPs). FAPs cells are responsible for defining the skeletal muscle tissue microenvironment. We have monitored their identity by their gene expression profiling at the single cell level. Here we accompany our bench protocol with bioinformatics analysis designed to process raw single cell gene expression data as well as to visualize the data. Our approach of single cell gene expression profiling is therefore a useful tool in the investigation the cellular heterogeneity and the contribution of the different cell subtypes to muscle homeostasis during healthy and diseased conditions.

Scientific Abstract:
Single cell gene expression profiling is a fundamental tool for studying the heterogeneity of a cell population by addressing the phenotypic and functional characteristics of each cell. Technological advances that have coupled microfluidic technologies with high-throughput quantitative RT-PCR analyses have enabled detailed analyses of single cells in various biological contexts. In this chapter, we describe the procedure for isolating the skeletal muscle interstitial cells termed Fibro-Adipogenic Progenitors (FAPs) and their gene expression profiling at the single cell level. Moreover, we accompany our bench protocol with bioinformatics analysis designed to process raw data as well as to visualize single cell gene expression data. Single cell gene expression profiling is therefore a useful tool in the investigation of FAPs heterogeneity and their contribution to muscle homeostasis.